

SEQUENCE LISTING

<110> UAB Research Foundation

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<120> METHODS AND COMPOSITIONS FOR IDENTIFYING
COMPOUNDS THAT INHIBIT HIV-1 SUBUNIT-SPECIFIC REVERSE
TRANSCRIPTASE

<130> 21085.0123P1

<140> Unassigned

<141> 2005-05-24

<150> 60/573,918

<151> 2004-05-24

<150> 60/668,858

<151> 2005-04-06

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1

gtttaaacgc	caccatggag	caggcccccg	aggaccaggg	ccccagagg	gagccccaca	60
acgagtggac	cctggagctg	ctggaggagc	tgaagagga	ggccgtgagg	cacttcccca	120
ggccctggct	gcacggcctg	ggccagcaca	tctacgagac	ctacggcgac	acctgggccc	180
gcgtggaggc	catcatcagg	atcctgcagc	agctgctggt	catccacttc	aggatcggct	240
gccagcacag	caggatcggc	atcatccagc	agaggagggc	caggaggaac	ggcgccagca	300
ggagctagtt	taaacactgc	acagagagac	aggctaattt	tttagggaaa	atgtggcctt	360
ccaacaaagg	gaggccaggg	aattttctcc	agaacaggcc	agagccaaca	gccccacccg	420
cagagagcct	cgggttcgga	gaggagatag	ccccctcccc	gaaacaagag	cgaaggaaa	480
aggagttata	ccccttaacc	tccctcaaat	cactctttgg	cagcgacccc	tagtcacagt	540
aagaataggg	ggacagctaa	tagaagccct	gttagacaca	ggagcagatg	atacagtgtt	600
agaagatata	aatttaccag	gaaaatggaa	acaaaaaatg	atagggggaa	ttggtggtct	660
tatcaaagta	agacagtatg	atcaaatact	tatagaaatt	tgtggaaaaa	aggctatagg	720
gacagtatta	gtaggaccta	cacctatcaa	cataattggg	agaaatatgt	tgactcagat	780
tggttggtact	ttaaattttc	caattagtcc	tattgaaact	gtaccagtaa	aattaaagcc	840
aggaatggat	ggtccaaa					858

<210> 2

<211> 96

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

Met	Glu	Gln	Ala	Pro	Glu	Asp	Gln	Gly	Pro	Pro	Arg	Glu	Pro	Tyr	Asn
1				5					10				15		
Ala	Trp	Thr	Leu	Glu	Leu	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Ala	Val	Arg
			20					25					30		
His	Phe	Pro	Arg	Val	Trp	Leu	His	Gly	Leu	Gly	Gln	His	Ile	Tyr	Glu
		35					40					45			
Thr	Tyr	Gly	Asp	Thr	Trp	Ala	Gly	Val	Glu	Ala	Ile	Ile	Arg	Ile	Leu
	50				55						60				
Gln	Gln	Leu	Leu	Phe	Ile	His	Phe	Arg	Ile	Gly	Cys	Gln	His	Ser	Arg
65					70				75						80
Ile	Gly	Ile	Thr	Arg	Gln	Arg	Arg	Ala	Arg	Asn	Gly	Ala	Ser	Arg	Ser
				85					90					95	

<210> 3

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

gtttaaacgc	caccatggag	caggcccccg	aggaccaggg	ccccagagg	gagccccaca	60
acgagtggac	cctggagctg	ctggaggagc	tgaagagggg	ggccgtgagg	cacttccccca	120
ggccctggct	gcacggcctg	ggccagcaca	tctacgagac	ctacggcgac	acctgggccc	180
gcgtggaggg	catcatcagg	atcctgcagc	agctgctgtt	catccacttc	aggatcggct	240
gccagcacag	caggatcggc	atcatccagc	agaggagggc	caggaggaac	ggcgccagca	300
ggagctagtt	taaac					315

<210> 4

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4

Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met
1				5					10					15	
Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys
			20					25					30		
Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser
		35					40					45			
Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys
	50				55					60					
Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu
65					70				75						80
Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His
			85					90						95	
Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly
			100					105					110		
Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr
		115					120					125			

Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160
 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
 165 170 175
 Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190
 Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His
 195 200 205
 Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
 245 250 255
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro
 260 265 270
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
 275 280 285
 Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
 290 295 300
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
 305 310 315 320
 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
 355 360 365
 Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
 370 375 380
 Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
 385 390 395 400
 Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
 405 410 415
 Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu
 420 425 430
 Pro Ile Val Gly Ala Glu Thr Phe
 435 440

<210> 5
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 5
 Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
 1 5 10 15
 Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys
 20 25 30
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
 35 40 45
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys
 50 55 60
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
 65 70 75 80

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Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
      85      90      95
Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
      100      105      110
Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
      115      120      125
Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
      130      135      140
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
      145      150      155      160
Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
      165      170      175
Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
      180      185      190
Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His
      195      200      205
Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu
      210      215      220
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
      225      230      235      240
Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
      245      250      255
Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro
      260      265      270
Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
      275      280      285
Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
      290      295      300
Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
      305      310      315      320
Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
      325      330      335
Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
      340      345      350
Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
      355      360      365
Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
      370      375      380
Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
      385      390      395      400
Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
      405      410      415
Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu
      420      425      430
Pro Ile Val Gly Ala Glu Thr Phe
      435      440

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<210> 6

<211> 170

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

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Lys Glu Gly His Gln Met Lys Glu Cys Thr Glu Arg Gln Ala Asn Phe
  1          5          10          15
Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu
      20          25          30

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Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg Cys
 35 40 45
 Gly Glu Glu Lys Thr Thr Pro Pro Gln Lys Pro Glu Gln Thr Asp Lys
 50 55 60
 Glu Leu Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Gln Arg Pro
 65 70 75 80
 Leu Val Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp
 85 90 95
 Thr Gly Ala Asp Asp Thr Val Leu Glu Asp Met Ser Leu Pro Gly Lys
 100 105 110
 Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg
 115 120 125
 Gln Tyr Asp Gln Ile Pro Ile Glu Ile Cys Gly His Lys Ala Ile Gly
 130 135 140
 Thr Val Leu Ile Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu
 145 150 155 160
 Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe
 165 170

<210> 7
 <211> 511
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 7
 aaaggaagga caccaaatga aagaatgcac tgagagacag gctaattttt tagggaaaat 60
 ctggccttcc cacaagggaa ggccagggaa ctttctccag agcagaccag agccaacagc 120
 cccaccagaa gagagcttca ggtgtgggga ggagaaaaca actccccctc agaagccgga 180
 gcagacagac aaggaactgt atcctttagc ttccctcaga tcactctttg gcaacgaccc 240
 ctcgtcacaa taaagatagg ggggcagcta aaggaagctc tattagatac aggagcagat 300
 gatacagtat tagaagacat gagtttgcca ggaaaaatgga agccaaaaat gataggggga 360
 attggagggt ttatcaaagt aagacagtat gatcagatac ctatagaaat ctgtgggcat 420
 aaagctatag gtacagtatt aataggacca acacctgtca acataattgg aagaaatctg 480
 ttgacacaga ttggttgcac tttaaatttt c 511

<210> 8
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 8
 Tyr Met Asp Asp
 1

<210> 9
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<220>
<221> VARIANT
<222> 2
<223> Xaa = any amino acid

<400> 9
Tyr Xaa Asp Asp
1

<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10
aagcccggga tggatggccc aaaagt

26

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11
tcctaaacgc gtctccctct aagctgctca atttacttag aaagt

45

<210> 12
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12
actttctaag taaattgagc agcttagagg gagacgcggt tagga

45

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13
tatgtcgaca cccaattatg aaaag

25

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 14
 tagatcagat ctgttgactc agattgggtg ca 32

<210> 15
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 15
 atctacacgc'gtttagaagg tttctgcgcc tt 32

<210> 16
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 16
 ttattaacgc gtccgcccct ctccctcccc cc 32

<210> 17
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 17
 ccatcccggtg ctttaatttt actggtacag tttcaatagg actaatgggt cccatgggtat 60
 tategtctt 69

<210> 18
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 18
 agcttgccctt gagtgcttca a 21

<210> 19
 <211> 26
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

ctgctagaga ttttccacac tgacta

26

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

ggctagctag ggaaccact g

21

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

atactgacgc tctcgaccc at

22